Adh14012 Human GPR
Adh39434 Cancer/an
Adh61810 Human GP
Adp12436 Human GPC
Adp12922 Protein e
Adp12929 Protein e
Adg95936 T cell ac
Adr67008 Human Can
Adr67008 Human Can
Adr67008 Human GPC
Ady50818 T cell ac
Adr6708 Human GPC
Ady6588 T cell ac
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Ady96588 T cell ac
Ady96588 T cell ac
Ady96588 Human G p
Add9598 Human G p
Add95388 Human mut

Human CXC Human che Human CXC

Protein e Protein e Human CXC T cell ac Human can

Human G p Human GPC

Human CXC Human GPR

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sub-fragment of the coding sequence was used as a probe to screen human cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two mew gene sequences were found that are clearly related to the IL-8 receptor. One of these was contained in clone Brr.9 and is predicted to encode an amino acid sequence which is 36* and 38* identical with the high and low affinity IL-8 receptor sequences, respectively. See also AAQ37107. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated human platelet factor 4 super-family receptor polypeptide and corresp. antibodies and DNA - useful as diagnostic and screening agents, and for treating inflammation or PF4AR-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-8 receptor cDNA sequence was isolated (see AAQ29505) and a 874bp
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pro-inflammatory cytokine, 8rr.9.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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monoclyte-like cell line HL-60 and human peripheral blood lymphocytes using a large fragment of IL-8 receptor DNA (full sequence given in AAQ80520). The mucleotide sequences of the 2 PF4ARs are given in AAQ80521 and AAQ80522, and their respective amino acid sequences in AAR68812 and AAR68813. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                 PVAITWCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
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100.0%; Pred. No. 1.8e-196;
ive 0; Mismatches 0;
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               Length 372;
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               100.0%; Score 1953; DB 2; 100.0%; Pred. No. 1.8e-196;
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Modulating interaction of a Burkitt's Lymphoma Receptor 1 polypeptide and
ligand, useful in drug screens.
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                                                                                                        (REGC ) UNIV CALIFORNIA
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                                                                                                                                    treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect inflammation. When immobilised, these antibodies may be used to detect purferlentkin-8 receptor B Expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lamma interleukin-8 considered blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See AAQ99006). (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
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                                        New antibodies against interleukin 8 type B receptor - used to treat prevent inflammation, also for detecting receptor expression and purificn.
                                                                                                                                 Antibodies directed against the interleukin-8 receptor B can be used
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 1953; DB 2; Length 372; 100.0%; Pred. No. 1.8e-196; ive 0; Mismatches 0; Indels 0
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                                                                                                        Example 2; Col 49-52; 62pp; English
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Matches 372; Conservative
                       N-PSDB; AAQ99009
                                                                                                                                                                                                                                                                                                Sequence 372 AA;
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invention relates to methods for modulating the interaction of BLR1 with its ligand, B lymphocyte chemoattractant (BLC, see AAY06642). The methods comprise combining BLR1 and BLC polypeptides with a candidate modulator agent under conditions whereby, but for the presence of the agent, the polypeptides engage in a first interation, and determining a second interaction of the polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the polypeptides. The modulator is preferably an antagonist, especially dominant negative, form of BLC. BLC and BLC agonists and antagonists may be useful for treating viral (e.g. HIV) infections, lymphoma, B lineage leukaemia, and autoimmune diseases such as rheumatoid arthritis, thyroiditis and diabetes
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This sequence represents human Burkitt's lymphoma receptor 1 (BLR1). The
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iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 372; Conservative
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Ното варіепв

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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in the diagnosis of tumors (especially colorectal disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchinal asthma or forbonic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, or endocrine, motor or urogenical systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antisathmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic.

Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (RR), which control migration and premise act or specific tumor set (RR), which control migration and premise act or specific tumor set (RR), which control migration and premise act or specific tumor set (RR), which control migration and premise act or specific tumor set (RR), which control migration and premise act or specific tumor set (RR), which control migration and premise act or specific tumor and inflammatory cells through a constellation of these cells. AAG800128 represent human chemokine
                                                                                                                                                               VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
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121 LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; merestasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiisthmatic; immunosuppressive; dermatological;
                                                                                  241 VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLANGSL
                                                      ALPEILFAKVSQCHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG80124 standard; protein; 372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-626256/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CXCR5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90673-AAY90683-AAY90683-AAY90683-AAY90683-AAY90683-AAY90683-AAY90683-AAY90683-AAY30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous proline in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and antagonists for a particular GPCR are useful for treating diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents a human wild-type GPCR referred to in an exemplification of
                                                                                                                                                                                              intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 152-153; 341pp; English.
                                                                                                                 Human G protein-coupled receptor BLR1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liaw CW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AREN-) ARENA PHARM INC
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                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                        antagonist.
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WPI; 2003-046718/04.
N-PSDB; ABZ42633.
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                                                                                                                                                                                                                                                                                 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
                                                                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoathritis; allergy; osteoprosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
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                                                                                        1 MNYPLTLEMDLENLEDLFWELDRYDDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
                                                                                                                              LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLL
                                                                                                                                                                       ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                              ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFISRFLYHVAGFLLPMLVMGWCYVG
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                                                                                                                    61 IFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
                                                           Gaps
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                                      Length 372;
                                                          Indels
fragments used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CXC chemokine receptor 5 protein SEQ ID NO:60.
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                                      Score 1953; DB 4;
Pred. No. 1.8e-196;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            ABP81789 standard; protein; 372 AA
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                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                          372
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                                    Query Match
Best Local Similarity 100.
Matches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                          SESENATSLITE
                   Sequence 372 AA;
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or cardidate polypeptide in a sample; and in the protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or gene therapy. The antigenic peptides for GPCRs, (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for cardiomy aminon-related diseases, immunological-related cell proliferative corresponding GPCRs. The antigenic peptides for treating immune-related diseases, or munuological-related cell proliferative diseases, or autoimmune diseases, eg. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, atheroscribritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute cinflammation, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis, ABZ42589 encode GPCR proteins given in ABP81675 to ABZ42289 encode ceremonic the present invention
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* isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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                                                                                                                                                                                                                   Disclosure, Fig 1, 523pp; English.
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                                                                                                                                      autoimmune diseases.
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The invention relates to a constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor (GPCR). The GPCR is used for screening therapeutic compounds as inverses agonists, agonists or partial agonists. The GPCR can be also be used to elucidate and understand the roles of GPCRs in normal and diseased humans. The GPCR need not be purified and isolated to be used to screen for therapeutic compounds. The utility of the GPCR as a research tool is enhanced because the role of a particular receptor can be understood before the endogenous ligand is identified. The present sequence is used in the exemplification
                                                                                                                                                                                                                                PVAITMCEFLGIAHCCLNPMLYTFAGVKERSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
                                                                                                                                              VYHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
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121 LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITGGTIMLVGFLL
                                                                                     ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                       ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; non-endogenous; G protein-coupled receptor; GPCR; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH14058 standard; protein; 372 AA.
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98US-0095677P.
98US-00170496.
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(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-801247/
N-PSDB; ADH14057.
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13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for reating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCR may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR reap be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a creening of compounds against orbina receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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                                                                                                                                                                       G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
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                                                                                                                                 Human G protein-coupled receptor (GPCR) polypeptide #19.
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                                                                                                                                                                                               intracellular-3 region; IC3; receptor
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        ADC22585 standard; protein; 372
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98US-00060188.
98US-0090783P.
98US-0095677P.
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Conservative 0
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                                                                                          (first entry)
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Best Local Similarity
Matches 372; Conserv
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14-APR-1998;
26-JUN-1998;
                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening for therapeutic agents useful in the treatment of haematological diseases, cancer, cardiovascular diseases, respiratory diseases and disorders of the peripheral and central nervous system in a mammal. The method of the
                                                                                                                                 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
                                                                                       I FLLGVIGNVLVLVI LERHRQTRSSTETFL FHLAVADLLLVFILDFAVAEGSVGWVLGTF
                                                                                                                                                               ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                          ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFISRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                       VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
                                                                                                                                                                                                                    VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
                                  MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
                                                                           IPLLGVIGNVLVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
                                                                                                                    LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiovascular; cytostatic; respiratory; CNS; central nervous system; gene therapy; haematological disease; cancer; cardiovascular disease; respiratory disease; CXC chemokine receptor 5; CXCR5; human.
              Gaps
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              Indels
   Pred. No. 1.8e-196;
Mismatches 0;
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    100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Local Similarity 100.
hes 372; Conservative
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transgenic mouse; neurological disorder; adrenal gland disorder;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; intestinal disorder; adrenal gland disorder;

colon disorder; blood disorder; immune disorder; bone disorder;

joint disorder; metabolic disorder; mutritive disorder; cancer;

kidney disorder; uterus disorder; nutritive disorder; cancer;

kidney disorder; uterus disorder; prostate disorder; breast disorder;

skin disorder; thyroid disorder; prostate disorder; settis disorder;

ktymus disorder; thyroid disorder; mitiparkinsonian; antimanic;

chymus disorder; antiinflammacory; vasotropic; antidiarrhoeic;

contral nervous system; respiratory; antidiarrhoeic;

virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

wimmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
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invention comprises contacting a test compound with a CXC chemokine receptor 5 (CXCR5) polypeptide or polyncleotide. The method of the invention is useful in screening for therapeutic agents that may be useful in treating the diseases mentioned above. The regulators of a CXCR5 are useful for regulating CXCR5 activity or for preparing a pharmaceutical composition for the treatment of the stated diseases in a mammal. The method and compositions are also useful in disapnosing and treating the stated diseases. The current sequence represents the human
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                                                                                                                                                                                                                                                                                                                                                                                       Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                   3; DB 8;
1.8e-196;
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1953;
100.0%; Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 SESENATSLITE 372
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                                                                                                                                                                                                                                                                                                                            Sequence 372 AA;
                                                                                                                                                                                                                                                             CXCR5 receptor.
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The present invention describes an isolated cancer associated (CA)

nucleic acid (I). Also described: (1) an expression vector comprising (1);

(2) a host cell comprising (I) or the expression vector; (3) a

microarray for detecting a CA nucleic acid; (4) an isolated cancer
associated protein (CAP) polypeptide, encoded within an open reading
frame of a CA sequence; (5) an isolated antibody, or its antigen binding
frame of a CA sequence; (5) an isolated antibody, or its antigen binding
frament, that binds to the above polypeptide; (6) a hybridoma that
produces the above monoclonal antibody; (7) a pharmaceutical composition
comprising the above antibody and a pharmaceutical accipient; (8) a kit
comprising the above antibody and a pharmaceutical accipient; (8) a kit
comprising the above antibody and a pharmaceutical accipient; (8) a kit
comprising cancer cells, comprising the (monoclonal) antibody
described above; (9) methods for diagnosing cancer or for detecting the
presence or absence of cancer cells in an individual; (11) a method for
chibiting gravit of cancer cells in an individual; (12) an
delivering a therapeutic agent to cancer cells in an individual; (12) an
electronic library comprising the above polynucleotide or polypeptide, or
                                               PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
                                                                                                                                                                                                                                                                VYHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                   ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; cancer associated nucleic acid; cancer associated cancer associated protein; CAP; cytostatic; vaccine; gene lymphoma; leukaemia; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; SEQ ID NO 18; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR66972 standard; protein; 372 AA.
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23-SEP-2003; 2003US-00669920.
15-DEC-2003; 2003US-00737318.
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                                                                                                                                                                                                                                                                                                                                                                              SESENATSLITE 372
                                                                                                                                                                                                                                                                                                                                               SESENATSLITF 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-652915/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
associated with GPCRs of the invention; methods of screening for
compounds useful in the treatment of GPCR-related diseases, a transgenic
compounds useful in the treatment of GPCR-related diseases, a transgenic
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the trasngenic mice; kits comprising several mice, each of which has
comprising a GPCR mucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
invention further discloses variants of the GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
discass including neurological discretes (e.g., Alzheimer's disease,
dispersion, diabetic neuropathy, Parkinson's disease or schizophrenia);
dispersion, diabetic neuropathy, Parkinson's disease or schizophrenia);
dispersion, diabetic neuropathy, Parkinson's disease or schizophrenia);
celles of the adrenal gland; disorders (e.g., angina, cardiac arrhythmia or
mycardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or
nycardial infarction); muscular disorders (e.g., auctoimmune disorders or
ADDS; bone and joint disorders (e.g., auctoimmune disorders or
conscribing and disorders (e.g., angina, prematoid
disorders of the kilment disorders (e.g., auctoimmune disorders or
conscribing and disorders of the kilment, prostate, testis, skin, stomach, pancreas, spleen, thymus and
thyroid (e.g., cancers). The full sequence data for this patent did not form part
cof the printed specification; those sequences not shown were obtained in
cof the printed spec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
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Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
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100.0%; Pred. No. 1.8e-196;
ive 0; Mismatches 0;
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                                                                                                                                                        09-SEP-2002; 2002US-0409303P.
                                                                                                     09-SEP-2003; 2003WO-US028226.
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                                                                                                                                                                                                                                       (PRIM-) PRIMAL INC.
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WO2004040000-A2.
                                                                                                                                                                                                                                                                                               Gaitanaris GA,
                                                  13-MAY-2004.
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their fragments; (13) methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CAP; (14) methods for detecting cancer associated with expression of a polypeptide in a test cell sample, or with the presence of an antibody in a test serum sample; (15) a method for treating cancers; and (16) a method for inhibiting the expression of CA gene in a cell. The CA sequences have cytostatic activity, and can be used in vaccines, and in gene therapy. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. They may also be used in screening for agents that modulate cancer. The present sequence represents a cancer associated protein (CAP) sequence, which is used in the exemplification of the present invention.
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                                                                                   IFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
                                                                                                                                  LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIMLVGFLL
                                                                                                                                                                                                                  181 ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                                                 ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                                                                                                                                                                VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
                                                                                                                                                                                                                                                                              PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL
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                     100.0%; Score 1953; DB 8; Length 372; 100.0%; Pred. No. 1.8e-196; ive 0; Mismatches 0; Indels 0
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                                               Conservative
                                 Best Local Similarity
Matches 372; Conserv
Sequence 372 AA;
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Human Burkitt lymphoma receptor homologue, SEQ ID NO:2243. ABB11873 standard; peptide; 378 AA. 11-JAN-2002 (first entry) ABB11873; RESULT 13 ABB11873

Human; cytokine; cell proliferation; cell differentiation; growth factor; inhibui; chemctaxis; chemckinesis; thrombolysis; oncogenesis; proliferation; metastasis; chemckinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; thumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; antiatethure; drug screening; gene therapy; antiinflammatory; antiatethmatic; antiarthritic; haemoscatic; antiatetiscleoclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.

IFLEGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF 120

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Homo sapiens

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contracted ABA08225-ABA09594 represent Listo novel numan polypeptides, and sequences ABA08225-ABA09594 represent inclead acids encoding them. The invention also relates to vectors and recombinant host cells comprising a mucleotide of the invention, methods of producing the novel polypeptides, and the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptides of the invention may contain therapeutic applications. The polypeptides of the invention may have activities; stem cell proliferation or cell have various activities; stem cell growth factor activity; chamber activities; stem cell growth factor activity; chamber activities; activities; hammer activities; catem cell growth factor activity; chamber activities; catem cell proliferation or metastasis. Chambolytic activities; activities; polypeptides and nucleotides of thrombolytic activities; activities; polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include regeneration and repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound repair growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound cepair growth. Polypeptides involved with tissue regeneration and fungal infections in addition to immune disease or accidental and themapeles involved with tissue regeneration cell growth. For example, such polyp
                                                                                                                                                                                                                                                                                                                                                                Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
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                                                                                                     05-FEB-2001; 2001WO-US003800
                                                                                                                                                03-FEB-2000; 2000US-00496914
27-APR-2000; 2000US-00560875
                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT
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                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                   WO200157188-A2
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                                                              09-AUG-2001
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ADC22719 standard; protein; 372
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98US-00060188.
98US-0090783P.
98US-0095677P.
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                                                                                                                                                                           Sequence 372 AA;
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14-APR-1998;
26-JUN-1998;
07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90643-AAY90643-Y90683-Y90683-Y90683-Y90683-Y90683-Y90683-Y90683-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083-Y9083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
antagonist; mutant; mutein.
                                               ALPEILFAKVSOGHHNNSLPRCTFSOENOAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                              VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
                                                                                                                                                                               PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL
                                                                                                                                                                                                                                              Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mutant G protein-coupled receptor BLR1 (V258K).
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N-PSDB; AAA30727.
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endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmacentrical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and alsorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAY90643-AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
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intracellular-3 region; IC3; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 1947; DB 3;
Pred. No. 7.5e-196;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7%; Pred. No. 7.5e
Matches 371; Conservative 0; Mismatches
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Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for constitutive activity.
     Chalmers DT;
     Behan DP,
                   WPI; 2003-742861/70
                          N-PSDB; ADC22718
     Liaw CW,
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Example 2; SEQ ID NO 200; 221pp; English.

The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TW6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutively cative cativity. The method is useful for creating a constitutively active correction of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR copyrides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCR polypeptides, which may be used to create a transgenic animal expressing the altered GPCR cay be used to create a transgenic animal expressing the altered GPCR cay be used to create a transgenic animal expressing the altered GPCR cay be used to create a transgenic animal expressing the altered GPCR cay be used to create a transgenic animal expressing the altered GPCR cay be used to create a transgenic animal expressing the altered GPCR cay may be used to create a gransgenic animal expressing the altered GPCR cay human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing accreaning of compounds against orphan receptors for which no ligand is a currently known. This sequence represents a human GPCR polypeptide of the

Sequence 372 AA;

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120
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                                                                                    MYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAXSL
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                                  Gaps
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99.7%; Score 1947; DB 7; Length 372; 99.7%; Pred. No. 7.5e-196; tive 0; Mismatches 1; Indels (
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                 Best Local Similarity 99.7 Matches 371; Conservative
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completed: August 29, 2005, 23:54:00 : 169 secs Search cor Job time

SESENATSLITE 372

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2005, 23:47:36; Search time 41 Seconds (without alignments) 872.991 Million cell updates/sec 1953
Sequence: 1953
Sequence: 1953
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Sequence: 1953
Sequence: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum Match 100*

Database: PIR 79:*
1: Pir::*
2: Pir::*
3: Pir::*
4: Pir::*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	G protein-coupled	MDCR15 protein - h	G protein-coupled	G protein-coupled	interferon-inducib	interleukin-8 rece	lymphocyte-specifi	G protein-coupled	G protein-coupled	interleukin-8 rece	interleukin-8 rece	interleukin-8 rece	fusin (LESTRA) - c	neuropeptide Y/pep	⋛	interleukin-8 rece	interleukin-8 rece	interleukin-8 rece		chemokine (C-C) re	7	chemokine (C-C) re	Φ	$\overline{}$	probable G protein	0	chemokine (C-C) re	ပ် (ပ	G protein-coupled
SUMMARIES	s ib	S	S56162	S42628	332785		A5361		A4568				: A53752									כי	æ	: I49339	כי	Н	: I38450	Ą	A45	\$55594
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	Match I	100.0	87.0	83.7	81.4	31.5	30.8	30.5	29.4	29.3	29.1	28.7	28.0	27.8	27.6	27.5	27.4	26.6	25.6	25.4	25.4	25.3	24.6	24.3	•	ë.	23.6	23.6	ë	23.0
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orphan G protein-c chemokine (C-C) re	G protein-coupled	G protein-coupled	MIP-1 alpha recept	G protein-coupled	angiotensin II rec	G protein-coupled	G protein-coupled	MIP-1 alpha recept	angiotensin II rec	probable chemoattr				
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371 362 356 359 371		receptor BL piens (man) 5 #sequence	; Emric 795-279 on-spec	· / 000	I PROT:	,Cross-references: GBB1136235, OMIM:60 Map position: 15q26.1-15q26.1 ,Superfamily: vertebrate thodopsin ,Keywords: G protein-coupled receptor;	vat	MOLENLI MOLENLI	NVLVLV NVLVLV	HKVNFY(KVSQGHI KVSQGHI	ORRPOR(ORRPOR(FLGLAHO FLGLAHO	SENATSLTTF 372
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244		1 in-c ies: 13-	ision IX, T Imm	sion sion s: p	ics:	-ret osit fami rds:	Mat Loca es			н н		0 0	m m	m
44441 12244 13244 1344		RESULT 1 S2667 G protein-coupled receptor BL C,Species: Homo eapiens (man) C,Date: 13-Jan-1995 #sequence	C;Acces R;Dobne Eur. J. A;Title	A; Keterner Annuer: S2600/; MULD: 93049015; FRID A; Accession: S26667 A; Status: preliminary A; MOlecule type: DNA a; Desciptus: 1-372, ADOR,	A; Gene: GDB:	A,Cross-reterences: GDB:136235; A,Map position: 15q26.1-15q26.1 C,Superfamily: vertebrate rhodol C,Keywords: G protein-coupled r	Query Match Best Local S Matches 372	රු සි	ò a	රු සි	රු සි	\$ g	රු සි	È

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RESULT 4
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G protein-coupled receptor - rat
G; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Accession: 532785
R; Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
FEBS Lett. 321, 173-178, 1993
A; Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is express A; Recession: 532785
A; Reseasion: 532785
A; Residuals: 1-374 - KOUD.
A; Residuals: 1-
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SLIFLLGHMGNILVLVILERHRHTRSSTEFFLFHLAVADLLLVFILPFAVAEGSVGWVLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TFLCKTVIALHKINFYCSSLLVACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 SLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRS 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YLSVAITLCEFLGLAHCCINPMLYTFAGVKFRSDLSRLLTKLGCAGPASLCQLFPNWRKS
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                                                                                                                                                                                                                                                                       MNYPLTLEMD--LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAY
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A; Cross-references: GB: L20332; NID: 9438798; PIDN: AAA16852.1; PID: 9438799
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                                                                                                                                Length 374;
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                                                                                                                            Query Match 83.7%; Score 1635; DB 2; Length 3 Best Local Similarity 82.9%; Pred. No. 8.3e-135; Matches 310; Conservative 29; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Indels
                                   C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane
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Best Local Similarity 81.0%; Pred. No. 6.9e-131;
Matches 303; Conservative 27; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSESENATSLTTF 372
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NyAlternate names: interleukin-8 receptor homolog; mubIRI protein

C;Specias: Mus musculus (house mouse)

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: $42628; C48909

R;Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.

Bur. J. Immunol. 23, 2532-2539, 1993

A;Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiatic

A;Reference number: $42628; MUID: 9409211; PMID: 8405054

A;Accession: $42628

A;Atatus: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-374 <KAI

A;Residues: 1-374 <KAI

A;Residues: UNIPROT: Q04683; EMBL: X71788; NID: 92598563; PIDN: CAA50673.1; PID: 9433

R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G

Genomics 18, 175-184, 1993

A;Title: Identification, chromosomal location, and genome organization of mammalian G-pr

A;Accession: (19909)

A;Accession: (19909)

A;Accession: (19909)
                                                                                                                                                                                        C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C; Accession: S56162
R; Barchen: J. : Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A; Title: Sequence variation of a novel heptahelical leucocyte receptor through alternation A; Accession: S56162; MUID:95366951; PMID:7639692
A; Accession: S56162
A; Accession: S56162
A; Accession: Joets acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-327 < ABRN-
A; Csoperfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 IHITCGTIWLVGFLLALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLA
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A;Residues: 151-269 <WIL>
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Pred. No. 1.6e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity
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A;Cross-references: UNIPROT:P25025; EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g5:A;Accession: 118712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
                                                                                                                                                                                    A;Molecule_type: DNA_
A;Residues: 6-360 <8PR>
A;Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 223, 1390-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 recept
A;Reference number: A39446; MUID:91368200; PMID:1891716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocyte-specific G protein-coupled receptor EBI1 - human NiAlternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1 Cispecies: Homo sapiens (man) cipecies: Homo sapiens (man) cipecies: 07-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 RRIV--YSSNVSPACYEDMGN--NTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLF 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 TEILGILHSCINPLIYAFIGQKFRHGLLKILAIHGLISKDSL----PKDSRPSFVGSSSG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MESDSFED-FWKGEDLSNYSYSSTLPPFLLDAAPCEPESLEINKYPVVIIYALVFLLSLL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 LHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 MDLENLEDLFWELDRLDNYNDTSLVENHLCPATE-GPLMASFKAVFVPVAYSLIFLLGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:127868; OMIM:146928
A;Map postition: 2435-2435
C;Superfamily: vertebrace rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.8%; Score 601.5; DB 2; 38.6%; Pred. No. 8.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: GDB: IL8RB; IL8RA
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A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon-inducible protein 10 (IP-10) receptor - mouse (;Specides: Mus musculus (house mouse) (;Specides: Mus musculus (house mouse) (;Specides: Musculus (house mouse) (;Accession: JE0349 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004 (;Accession: JE0349 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004 (;Accession: JE0349 Ke; Narumi, S. Biochem. Biophys. Res. Commun. 251, 41-48, 1998 #s. Biochem. Biophys. Res. Commun. 251, 41-48, 1998 #s. Biochem. Biophys. Res. Commun. 251, 41-48, 1999 #s. Biochem. Biophys. Res. Commun. 251, 41-48, 1999 #s. Biochem. JE0349 #s. MulD:99009219; PMID:979094 #s. Reseidus: JE0349 #s. MulD:99009219; PMID:979094 #s. Residus: 1-367 <TAM> A;Residus: 1-367 <TAM> A;Residus: 1-367 <TAM> A;Residus: Inis protein is important for lymphocyte trafficking to lymphoid organs. C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-8 receptor type B - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004 (Speciesion: 137888; 138712; A5361; A39446 (Speciesion: 137888; 138712; A5361; A39446 (Speciesion: Lohem. 269, 2694) (P.M. A. Tiffany, H.L.; Murphy, P.M. A. Biol. Chem. 269, 2694 (B1987) (P.M. A) 
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                                                              358
                                                                                                                                                                                           301 YLSVAITLCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCAGPASLCQLFPGWRKS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 QVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LVSRGQRRFRAMRLVVVVVAAA 262
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                             VGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG
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Best Local Similarity 38.8%
Matches 134; Conservative
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C; Keywords: G protein-coupled receptor; transmembrane protein
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Best Local S
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       Cyaccession: 155/51; Bayort, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor A; Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Accession: B55735
A;Residues: L-378 <-SCH>
A;Residues: L-378 <-SCH
A;Residues: S52443
A;Reference number: S52443
A;Accession: S52443
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A;Accession: S52443
A;Accession: S52443
A;Accession: S52443
A;Conserreferences: GDB:342065; OMIM:600242
A;Genetics: C;Genetics: GDB:342065; OMIM:600242
A;Genetics: Type: DNA
A;Cross-references: GDB:342065; OMIM:600242
A;Genetics: C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Date: 21-Sep-1993 #sequence_revision 19-Sep-1993
C; Date: 21-Sep-1993 #sequence_revision 19-Sep-1993
C; Superimental Special Novel 19-Sep-1993
C; Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 IFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAG 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 VKFRSDLSRLLTKLGCTGPASLCQLFPSW-----RRSSLS-ESENATSLT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%; Score 596; DB 2; Length 378;
36.8%; Pred. No. 2.7e-44;
tive 77; Mismatches 123; Indels
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Best Local Similarity 36.8%
Matches 129; Conservative
 Accession: B55735; S52443
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A55735
G procies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled recept
A;Reference number: A55735; MUID:95154835; PMID:7851893
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A, Molecule type: mRNA
A, Redues: 1-378 < SCA.
A, Cross-references: UNIPROT: P47774; GB: L31580; NID: 9468340; PIDN: AAA74232.1; PID: 9468: C, Superfamily: vertebrate rhodopsin
C, Superfamily: vertebrate rhodopsin
C, Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                         89 FLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRY 148
                                                                                                                                                                                                                                                          96 YLLNLAVADILFLITLPFWAYSAAKSWVFGVHFCKLIFAIYKWSFFSGMLLLCISIDRY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 IHITCGTIWLVGFLLALPRILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 GFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVALLVTSIPPLCWSPYHIVIFLDTLA 285
                                                                                                                                                                                                                                                                                                                                           LAIVHAVHAYRHRR--LLSIHITCGTIWLVGFLLALPEILFAKVSQGHHNNSLPRCTFSQ 206
                                                                                                                                                                                                                                                                                                                                                                               48 SFKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 NFNITNSSCETSKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 RLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGP 345
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                                                                                                                                               29 DISLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 ENGAETHAWFISRFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 IFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAG
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 VKFRSDLSRLLTKLGCTGPASLCQLFPSW-----RRSSLS-ESENATSLT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                        22;
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; Score 574; DB 2; Length 370; Pred. No. 2.2e-42; 78; Mismatches 125; Indels
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Query Match 29.4%; Best Local Similarity 35.9%; Matches 126; Conservative 7
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A; Molecule type: DNA
A; Readdues: 1-150 < RES.
A; Residues: 1-150 < RES.
A; Cross-references: UNIPROT: P25024; EMBL: X65858; NID: 9312046; PIDN: CAA46688.1; PID: 93.
B; Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389; 139.
A; Title: Comparison of the genomic organization and promoter function for human inter.
A; Reference number: 137898; MUID: 95014476; PMID: 7929358
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C;Species: Oryctolague cuniculus (domestic rabbit)
C;Dates: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53752
R;Prado, G.N.; Thomas K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava J. Balol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-16 <RE3>
A; Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R; Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A; Title: Structure and functional expression of a human interleukin-8 receptor.
A; Reference number: A39445; MUID:91368199; PMID:1840701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S3 SLIGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFPALTLPIWAASKVNGWIFGTFLCKV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VIALHKWNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 ILFAKVSQGHHNNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLLPMLVMGWCYVGVVH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 ITMCEFLGLAHCCLNPMLYTPAGVKFRSDLSRLLTKLGCTGPASLCQ-LFPSWRRSSLSE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 RLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVA
                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: U11870; NID: 9511804; PIDN: AAA64378.1; PID: 9511805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reaidues: 1-275,'T',277-350 <HOL>
A;Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GDB:135039, OMIM:146929
A,Map position: 2435-2435
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 561; DB 2;
Pred. No. 2.8e-41;
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                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                               A; Accession: I38710
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A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994; PMID:1898400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1.355 < BEC>
A; Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
A; Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
A; Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
A; Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor. A; Reference number: A46483
A; Reference number: A46483
A; Residues: Preliminary
A; Molecule type: mRNA
A; Residues: 1-355 < LEE>
A; Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A; Experimental source: neutrophils
A; Experimental source: neutrophils
A; Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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NyAlternate names: interleukin-8 receptor, high-affinity
C;Species: Homo sapians (man)
C;Date: 22-Jan-1993 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: 137449; 138710; I38711; A39445
R;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A;Title: The high-affinity interleukin 8 receptor gene (ILBRA) maps to the 2q33-q36: A;Reference number: 137449; MUID:93252387; PMID:8486366
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                                                                                                                                                                                                                          interleukin-8 receptor - rabbit
C;8pecíse: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JQ1231; A46483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.1%; Score 569; DB 2; Length 355; Best Local Similarity 38.3%; Pred. No. 5.6e-42; Matches 129; Conservative 52; Mismatches 146; Indels 10; Gaps
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ASLCQLFPSWRRSSLSESENATSLTTF 372
                                        A; Molecule type: DNA
   346
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                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 c.PRA>
A;Cross-references: UNIPROT:P35344; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                          LGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCK 123
                                                                                                                                                                                                                                                                                                                                                                                                               124 TVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VVSLVKEVNFYSGILLLACISVDRYLAIVHATRTMIQKRHL-VKFICLSMWGVSLILSLP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 EILFAKVSQGHHNNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLLPMLVMGWCYVGVV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSLSE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 ASFKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USENTRA) - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: G00048
R;Tatsumi, M.
submitted to GenBank, July 1996
A;Reference number: H00048
A;Reference conneber: H00048
A;Accession: G00048
A;Accession: G00048
A;Accession: G00048
A;Residues: 1-352 crAT>
A;Residues: 1-352 crAT>
A;Residues: 1-352 crAT>
A;Coss-references: UNIDROT: Q28474; GB:D86579; NID:g1468948; PID:g1468949
C;Superfamily: vertebrate rhodopsin
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larity 34.2%; Pred. No. 1e-39;
Conservative 69; Mismatches 124; Indels
                                                                                                                                                                       Query Match 28.0%; Score 547; DB 2; Length 358 Best Local Similarity 37.2%; Pred. No. 4.7e-40; Matches 137; Conservative 50; Mismatches 163; Indels
A; Reference number: A53752; MUID: 94230294; PMID: 8175642
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Matches 113; Conserv
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DD 219 TELDITARIANOMPTCLANSCHAMPRIAGENIESTICANSCHAMPRIATION 258
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94 WAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLT 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 DNYNDTSLVENHL-----CPATEGPLMASFKAVFVPVAYSLIFLLGVIGNVLVLVILER
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Mismatches 124; Indels
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70;
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Search completed: August 29, 2005, 23:57:44 Job time : 42 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at: http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or nembers of the public who may encounter UniProt temporary accession

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IsoId=P12302-2; Sequence=VSP_001892;
TISSUE SPECIFICITY: Expression in mature B-cells and Burkitt
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IsoId=P32302-1; Sequence=Displayed;
                                                                                                                                                                                                                                                              STANDARD;
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NCBI_TaxID=9606;
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CCR5 RAT
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xenopus lae
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nycticebus
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Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
Sequence variation of a novel heptahelical leucocyte receptor through
alternative transcript formation.";
Biochem. J. 309:773-779(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
C-X-C chemokine receptor type 5 (CXC-RS) (GXCR-S) (Burkitt'S lymphoma receptor 1) (Monocyte-derived receptor 15) (MDR15).
                                                                                                        xenopus
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MEDIJINE=93049615; Pubmed=1425907;
Dobner T., Wolf I., Emrich T., Lipp M.;
Differentiation-specific expression of a novel G protein-coupled receptor from Burkitt's 1ymphoma.";
Eur. J. Immunol. 22:2795-2799(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Q6in95
Q8n6t6
Q9dgil
Q7zxj7
Q8qfr5
P55920
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SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                        372 AA
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                               118A GORGO
Q61N<sup>9</sup>5
Q8N6T6
Q9DG11
Q9CXJ7
Q8QFR5
118A PANTR
Q9MZM2
ILBA HUMAN
Q9YGC3
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Q9MZM4
Q93237
Q93247
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SEQUENCE FROM N.A. (ISOFORM SHORT)
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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last seq
25-0CT-2004 (Rel. 45, Last ann
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05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                            Burkitt lymphoma receptor
                                                                                361 SESENATSLITF 372
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Matches 311; Conservative
                                                                                                                                                                PRELIMINARY;
                                                                                                     361 SESENATSLITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensent is commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                            MIM) 601613; -. 601613; -. 601613; -. 601613; -. 601613; -. 601613; -. 601613; -. 601613; -. 60161938; Cintegral to plasma membrane; TAS. 601601938; Fig-protein coupled receptor activity; TAS. 601600188; Fig-protein coupled receptor protein signalin. . .; TAS. 6016191; PR000188; Angtuz receptor. InterPro; IPR001053; CXC 5 receptor. InterPro; IPR001053; CXC 5 receptor. InterPro; IPR001053; CXC 5 receptor.
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PRINTS; PR00241; ANGIOTENSIR.

PRINTS; PR00241; ANGIOTENSIR.

PRINTS; PR00237; GPCRH4DODESN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

Alternative splicing; B-cell activation; G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.

DOMAIN 1 55 Extracellular (Potential).
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Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Sypoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

N-linked (GlcNAc. . ) (Potential).

N-linked (GlcNAc. . ) (Potential).

Notential.

Missing (in isoform Short).
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G -> S (in dbSNP:665648).
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6DF84C839492ACCF CRC64;
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Pred. No. 1.4e-125;
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EMBL, X68829; CAA48723.1; -.
PIR, S26667; S26667.
Genew, HGNC:1060; BLR1.
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STATN=C57BL/64) TISSUE-Wammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=110.1073/pnas.242603899;
Altachener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Bonelow S.I., Wang J., Hebte F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brange C., Stepleton M., Soares M.B., Bonaldo M.F., Casrvinci P., Prange C., Stepleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., McDwan P.J., McKernan R.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Kettemenn M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko X., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Reperation and initial analysis of more than 15,000 full-length human
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241 VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064059; AAH64059.1;
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0007515; P:lymph gland development; IMP.
InterPro; IPR0010548; Anglan2_receptor.
InterPro; IPR001053; CXC 5_receptor.
InterPro; IPR0010576; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PRINTS; PR00241; ANGIOTENSINR.
PRINTS; PR00254; ACCHMKINERS.
PRINTS; PR00237; GPCRH4DODESN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; UNKNOWN 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 AA.
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STRAIN=C57BL/6J; TISSUE=Mammary gland;
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B-cell activation;
Transmembrane.
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                   TFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIMLVGF
                                                                                                                                                                       LFALPELLFAKVGQPHNNDSLPQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCY
                                                                                                                                                                                                                                                                                                         VGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG
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                                                                           SLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLG
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 MNYPLTLEMD--LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (Burkitt'S lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 151-269 FROM N.A.
TISSUB-TEETLS;
MEDLINE=94116980; PubMed=8288218;
Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
Copeland N.G., Jenkins N.A.;
Tidentification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
Genomics 18:175-184(1993).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=BALBLOC, TISSUE-Liver;
STRAIN=BALBLOC, TISSUE-Liver;
MEDLINE-9400921; PubMed=8405054;
Kaiser E., Foerster R., Wolf I., Epensperger C., Kuehl W.M.,
"The G protein-coupled receptor BLR1 is involved in murine B
differentiation and is also expressed in neuronal tissues.";
Eur. J. Immunol. 23:2532-2539(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98146056; PubMed=9486651; DOI=10.1038/35876; Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G., Williams L.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor 1 homolog).
Name=Blr1; Synonyme=Cxcr5, Gpcr6;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 1 MNYPLTLEMD - LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAY TFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGF LLALPEILFAKVSQGHHINNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCY B-cell chemostractant (BLC). Involved in B-cell migration into B-cell chemostractant (BLC). Involved in B-cell migration into B-cell follicles of spleen and Peyer's patches, but not in those of mesentric or peripheral lymph nodes.

-! SUBCELLIARAR LOCATION: Innegral membrane protein.
-! TISSUB SPECIFICITY. Mainly in spleen, in rething B-cells.
-! SIMILARITY: Belongs to the G-protein coupled receptor 1 family. R EMBL; L2032; AAA16852.1; -..
R PIR; \$42628; BAZ.
R MGD; MGI.103567; BLY.
R InterPro; IPR000248; AAGPINZ receptor.
R InterPro; IPR000248; ANGRINZ receptor.
R InterPro; IPR000157; CXC 5 receptor.
R InterPro; IPR00017; TYM_1; J.
R RINTS; PR00241; ANGIOTENSINR.
R PRINTS; PR00244; ANGIOTENSINR.
R PRINTS; PR00254; GPCRHHODOPSN.
R PRINTS; PR00237; GPCRHHODOPSN.
R PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
R PROSITE; PS0262; GFROTEIN RECEP F1 2; 1.
R PROSITE; PS0262; GFROTEIN COUPLED receptor; Glycoprotein; made in lymphoid follicles activates Cycoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential) 83.7%; Score 1635; DB 1; Length 374; 82.9%; Pred. No. 7.1e-104; Extracellular (Potential).

1 (Potential).

2 (Potential).

Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).

6 (Potential).

7 (Potential).

6 (Potential).

7 (Potential).

8 (Potential).

9 (Potential).

10 (Potential).

11 (Potential). Indels 385258420C1EDE30 CRC64; 33, 29; Mismatches Potential "A B-cell-homing chemokine made i Burkitt's lymphoma receptor-l."; Nature 391:799-803(1998). 42100 MW; EMBL; X71788; CAA50673.1; -. Query Match Best Local Similarity 82.9³ Matches 310; Conservative

118

9

180

300

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61 SLIFLLGMMGNILVLVILERHRHTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLG 120
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EMBL, AR023969, AAC23950.1, -.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0016493; F:C-C chemokine receptor activity; IEA.

GO, GO:0016494; F:C-C chemokine receptor activity; IEA.

GO, GO:0004842; F:C-C chemokine receptor activity; IEA.

GO, GO:0001884; F:receptor activity; IEA.

GO, GO:0001886; F:receptor activity; IEA.

GO, GO:0001886; F:receptor activity; IEA.

GO, GO:0001886; F:receptor activity; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
N'linked (GlonAc. . .) (Potential).
N-linked (GlonAc. . .) (Potential).
                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                       Length 374;
                                                                                                                                                                                                                                                                42; Indels
                                                                                                                                                                                 D87A3AC816207319 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                       0; DB 1;
8.4e-101;
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                                                                                                                                                                                                                                                                27; Mismatches
                                                                                                                                                                                                                       Score 1590;
Pred. No. 8.
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MEDLINE=98244380; PubMed=9584981;
                                                                                                                                                                                 42012 MW;
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81.0%;
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01-NOV-1998 (TrEMBLrel. 08,
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                                                                                                                                                                                                                                            Similarity
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                                                           DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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DISULFID
SEQUENCE
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                                                                                                   <u>i</u>8
                                                VGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG
                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
25-007-2004 (Rel. 45, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma receptor 1 homolog) (Neurallymphatic receptor) (NLR).
Name=Blr1; Synonyms=Cxcr5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93238948; PubNed=8386678; DOI=10.1016/0014-5793(93)80102-Z; Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.; Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.; Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.; MLR) which is expressed in neuronal and lymphatic tissue."; PEBS Lett. 321:173-178(1993).

-I- FUNCTION: Cytokine receptor that binds to B lymphocyte chemoattractant (BLC) (By similarity).

-I- SUBCELLIGAR LOCATION: Integral membrane protein.

-I- TISSUE SPECIFICITY: Expressed in neuronal and lymphatic tissue.

-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00241; ANGIOTENSINR.
PRINTS; PR00241; ANGIOTENSINR.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN PECEP_F1_1; 1.
PROSITE; PS00262; G PROTEIN RECEP_F1_2; 1.
B-cell activation; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular (Potential).
1 (Potential).
Cyroplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                               374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000248; Angtn2_receptor.
InterPro; IPR001053; CXC_5_receptor.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X71463; CAA50582.1; -.
                                                                                                                                                                                                             SLSESENATSLITE 372
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S32785; S32785.
RGD: 62010; Blr1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                         239
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7

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LOC443669 protein (Fragment).
Name=LOC443669;
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                                                                                                                                                           Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               329
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                                                                                                                                    Query Match
                                                                                                                                                 Local
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                                                                                                                                                                                                   107 TTTENFLFHLTLANLALLLTFFFSVVSSLAGWVFGTFLCKILSAVHKINFYLHEHAAGLH 166
                                                                                                                                                                                                                                                                                                                                                                    FSQENQAETHAWFISRFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAIL 263
                                                                                                                                                                                                                                                                                                                                                                                                          VTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYT 323
                                                                                                                                                                                                                                                                                                                                                                                                                         284 VTGVFLLCWSPYHIVIFINTLTKLEAFAKDCLLEDHLDTAIMVTEAIGFTHCCLNPIIYA 343
                                                                                                                                                                                        83
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-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

EMBL; ABO99931; BAC55184-1;
-0. GO:0016493; F:C-C chemokine receptor activity; IEA.

GO; GO:0016493; F:C-C chemokine receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:G-protein coupled receptor protein signalin. .; IEA.
                                                                                                                                                                                                                                                                                                               167 RVDRYLAIVYAIHTYRKARARSIHLTCTAIWLSSLLLTLPDLIFMEVWTDESNRSI--CY
                                                                                                                                                                                                                                            84 SSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACI
                                                                                                                                                                                                                                                                                                 144 AVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKVSQGHHNNSLPRCT
                                                                                                                                                                                       28 NDTSLVENHLCPATEGPLMAS ---- FKAVFVPVAYSLIFLLGVIGNVLVLVILERHROTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Regulation of Blastocyst Migration, Apposition, and Initial Adhesion
by a Chemokine, Interferon {gamma}-inducible Protein 10 kDa (IP-10),
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22765629; PubMed=12756249; DOI=10.1074/jbc.M300470200;
Nagaoka K., Noljma H., Watanabe F., Chang K.T., Christenson R.K., Sakai S., Imakawa K.;
                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||||||| || ||||| 344 FIGVKFRNDFFRILHELGCISQETLQEILEVTRKGCGIESDNTTSISTF 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 FAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSLSESENATSLTTF 372
                                                                                                                                 Length 392;
                                                                                                                                 Query Match

44.4%; Score 866.5; DB 2; Length
Best Local Similarity 48.4%; Pred. No. 2.1e-51;
Matches 169; Conservative 57; Mismatches 116; Indels
                                                                                                        392 AA; 44760 MW; 3B5CFCE88366F088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                    PRINTS; PRO0657; CCCHEMOXINER.
PRINTS; PRO0564; CXCCHMKINERS.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000355; Chmkine_receptor.
Interpro; IPR004070; CXC_3_receptor.
InterPro; IPR001053; CXC_5_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     during Early Gestation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXC chemokine receptor 3.
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                         Pfam; PF00001; 7tm 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=cxcr3;
                                                                                            Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 PLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 ALCWTPYHLVVLVDTLMDLGALARNCGRESRVDVAKSVTSGMGYMHCCLNPLLYAFVGVK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1.4., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., John M., Moore T., Max S.I., Wang J., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyvik S., Carninci P., Prange C., Bran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley N.C., Hale S., Garcia A.M., Gabbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHLAVADLLLVPILPFAVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPRILFAKVSQGHHNNSL--PRCTFSQEN
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                               Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRSDLSRLLTKLGCTG-----PASLCOLFPSWRRSSLSESENAT 367
                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 646; DB 2; Length 36
40.8%; Pred. No. 2.2e-36;
ive 54; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222AE9D136E09C0F CRC64;
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001, 7tm 1; 1.
PRINTS; PR00657; CCCHEMOKINER.
PRINTS; PR01637; CXCCHEMKINER3.
PRINTS; PR01637; GPCRRHODOPSN.
PRINTS; PR01637; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
G-BROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 366 AA; 40870 MW; 222AB9D136E09C0F CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Name=CXCR3; Synonyms=GPR9;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 29:335-344 (1995)
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                             FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                            Mammalia, Euther
NCBI TaxID=9606
                                                                                                                                                 and expression
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                                                                          SEQUENCE
 antigen)
'n.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 FDRRFLPAFYSIVFLLGMLGNVLVLVVLLQNRWRLQSTDIFLLHLALADILLVVTLPFWA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 MNILAVLPDNCTTDSNIDIALSVTSGLCYFHSCLNPLLYAFVGAKFRAKLVBLLNKLSCI 359
                                                                                                                                                                                                                  GO:0016021; Cintegral to membrane; IEA.
GO:0016493; F:C-C chemokine receptor activity; IEA.
GO:0016494; F:C-X-C chemokine receptor activity; IEA.
GO:0001584; F:C-X-C chemokine receptor activity; IEA.
GO:0001584; F:C-X-C chemokine receptor activity; IEA.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
          Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTIWLVGFLLALPEILFAKVSQGHHNNSLPRCTFS----QENQAETHAWFTS-RFLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IVGFLIPLCFMVYCYTHIIHSLCQTHGF-KKQKALRVVIAVVVIFFLCMTPYNIVALLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Gaps
                                                                 TISSUE=Spleen;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
MEDLINES.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.,
Richardson P.,
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CD183
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCR3 HUMAN STANDARD, PRT; 368 AA.
P49682, 015185; Q9P2T4; Q9P2T5;
01-PEB-1996 (Rel. 33, Created)
01-W0-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
C-X-C chemokine receptor type 3 (CXC-R3) (CKR-L2)
                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Mismatches 118; Indels
                                                                                                                                                                                Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073571; AAH73571.1; -
                                                                                                                                                                                                                                                                                                                                                                                            390 AA; 44470 MW; 44294060B6DCA92D CRC64;
                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                             Pfam; PP00001; 7cm 1; 1.
PRINTS; PR00657; CCCHEWOKINER.
PRINTS; PR001532; CXCCHMKINER3.
PRINTS; PR010237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                   32.7%; Score 638.5; DB 2
39.8%; Pred. No. 7.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPQIVKKYIKYNPPAKPSTWSESGDTT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 GPASLCQLF---PSWRRSSLSESENAT 367
                                                                                                                                                                                                                                                                            InterPro, IPR000355; Chmkine receptor.
InterPro, IPR004070; CXC 3 receptor.
InterPro, IPR000276; GPCR Rhodpsn.
                                                                                                                                    Dev. Dyn. 225:384-391(2002)
                     mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
 Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                           SEQUENCE FROM N.A.
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                        rissum=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                         130;
                                                                                                                          initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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MR ManeackCR3; SynonymaeCR89;

Remon saptem (Human)

Remon saptem
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147; Conservative
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                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                        Name=GPR9;
                                                                                                             131
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
GO; GO:0001955; P:cell adheaton; TAS.
GO; GO:0006928; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
InterPro; IPR000455; Chmkine zeceptor.
InterPro; IPR004070; CXC 3 receptor.
InterPro; IPR004076; GRC 3 receptor.
"Interferon-inducible T cell alpha chemoattractant (I-TAC): a novel non-ELR CXC chemokine with potent activity on activated T cells through selective high affinity binding to CXCR3.";
J. Exp. Med. 187:2009-2021(1998).
-!- FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC.
-!- SUBCELLIARA LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- DATABASE: NAME=PROW; NOTE=PROW 1:78-83(2000);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/650534941_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
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2 (Potential).
Extracellular (Potential).
3 (Potential).
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
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A -> R (in Ref. 2).
F08A3B44B2BBAD04 CRC64;
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Cytoplasmic (Potential).
By similarity.
N-linked (GlcNAc. . .) (F
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Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTIG=VAR_016240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
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EMBL; Z79783; CAB02143.1; ALT_INIT.
                                                                                                                                                                                                                                          EMBL; U32674; AACDODODO,
EMBL; AB032735; BAA92297.1; -
EMBL; AB032736; BAA92298.1; -
Genew; HGNC:4540; CXCR3.
                                                                                                                                                                                                                      AY242128; AAO92295.1; -- BC034403; AAH34403.1; --
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203
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292
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Best Local Similarity
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A MADLINE-Z2068/1; Prancalancia (C.) Mazzinghi B., Orlando C., Maggi E., Marra F., Cosmi L., Francalanci C., Mazzinghi B., Orlando C., Maggi E., Marra F., Cosmi L., Segrinati C., Mazzinghi B., Orlando C., Maggi E., Marra F., Romagnani S., Serio M., Romagnani P. CxCR3 mediates the inhibition of an alternatively spliced variant of CXCR3 mediates the inhibition of an alternatively spliced variant of CXCR3 mediates the inhibition of an alternatively spliced variant of CXCR3 mediates the inhibition of an alternatively spliced variant of CXCR3 mediates the inhibition of an alternatively spliced variant of CXCR3 mediates the inhibition of an alternatively spliced variant of GXCR3 mediates as a functional receptor factor 4.";

The Massimal CXCRTION: Integral membrane protein (By similarity).

EMBL: AF466935; AAF5581.1; -.

BRMS: AF466935; AAF5581.1; -.

CXCR3 mediates and coupled receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRRO0276; GPCR_Rhodpsn.

PROSITE; PSO0237; GPROTEIN RECEP [1.1; 1.)

PROSITE; PSO0227; GPROTEIN RECEP [1.2; 1.]

CM G-protein coupled receptor; Faceptor; Transmembrane.

SQUENCE 415 AA; 45522 MW; 325C8A65982A43C4 CRC64;
8
                                                                                                                                                                                                                                                                                      71 LVLVILERHROTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                                                        VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 GLGYMHCCLNPLLYAFVGVKFRERMMLLILIRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 364
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                                                                                                                              20 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFURAFLPALYSLLFLLGLLGNG
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                                                                                    11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORRPOROKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
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Gaps
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
    18;
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    Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CXC chemokine receptor transcript variant B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 AA
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    20;
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                                                                                      208 QVGRT----ALRVLQLVAGFLLPFLVMAYCYAHILAVL-LVSKGQRRFRAMRLVVVVVAA 262
                                                                                                                                                                                                    263 FAVCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLYAFVGV 322
                                                                                                                                                                      268 PFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGV 327
149 YLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFALPDFIYLSANYDQRLNA-THCQYNFP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINES 9818636; bubMed=9653165; DOI=10.1073/pnas.95.14.8205;
Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Hedrick J., Zlotnik A.;
Jenkins N.A., Hedrick J., Zlotnik A.;
The CC chemokine 6Kine binds the CKC chemokine receptor CXCR3.";
Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
-!- PUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC (By similarity). Binds to SCYB3/MIG, SCYB10/INP10 and SCYB11/ITAC (BY SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral
                                                        208 NQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMED; AF045146; AND.
R MGD; MGI:1277207; Cxcr3.
R InterPro; IPR004070; CXC.3 receptor.
R InterPro; IPR004076; CXC.3 receptor.
R InterPro; IPR004076; GPCR. Anodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHONDOPSN.
DR PROSITE; PS00237; GPROTEIN RECEP. FI. 1; 1.
DR PROSITE; PS00237; GPROTEIN RECEP. FI. 2; 1.
DR PROSITE; PS00237; GPROTEIN RECEP. FI. 2; 1.
DR PROSITE; PS00237; GPROTEIN RECEP. FI. 2; 1.
THE G-protein coupled receptor; Glycoprotein; Transmembrane.
The coupled receptor; Glycoprotein; Transmembrane.
The coupled receptor; Glycoprotein; Potential).
                                                                                                                                                                                                                                                                                                                        323 KFREGMWMLFTRLGRSDQRGPQR--QPSSSRRESSWSETTEASYL 365
                                                                                                                                                                                                                                                                                    KPRSDLSRLLTKLGCT---GPASLCQLFPSWRRSSLSESENATSL 369
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
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2 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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25-OCT-2004 (Rel. 45, Last annotation update)
C-X-C chemokine receptor type 3 (CXC-R3) (CXCR-3).
Name=Cxcr3; Synonyms=Cmkar3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
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  120 AVAAVLLSRRTALSSTDTFLIHLAVADTLIVLTLPLWAVDANQWVFGSGLCKVAGALFN 179
                                                                                      VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                              237
                                                                                                                                                                                                       191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tamaru M., Tomingag Y., Yatunami K., Natumi S.;

"Cloning of the murine interferon-inducible protein 10 (IP-10)

"Cloning of the murine interferon-inducible protein 10 (IP-10)

I receptor and its specific expression in lymphoid organs.";

Biochem. Blophys. Res. Commun. 251:41-48(1998).

- :- SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).

C. :- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

R EMBL; AB0031144; BA34045.1; -.

R MGD; MGI:1277207; Cxcr3.

R GO; GO:0016021; C:integral to membrane; TAS.

R InterPro; IPR000355; Chmkine_receptor.

R InterPro; IPR000470; CxC 3_receptor.

R InterPro; IPR000470; CxC 3_receptor.
                                                                                                                          -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                      309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 NESDFSDSPPCPQ---DFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TEBMBLrel. 13, Last sequence update)
01-MAX-2000 (TEBMBLrel. 26, Last annotation update)
101-MAR-2001 (TEBMBLrel. 26, Last annotation update)
Interferon-inducible protein 10 receptor.
Name=Cxcr3; Synonyms=MxXR3;
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Blood;
MEDLINE=99009219; PubMed=9790904; DOI=10.1006/bbrc.1998.9404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERM; PP00001; 7tm 1; 1.

PRINTS; PR00557; CCCHEMOKINER.

PRINTS; PR01532; CXCCHMKINER3.

PROSITE; PS00237; GPRCRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;
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Best Local Similarity
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARIN: Belongs to family 1 of G-protein coupled receptors.

EMBL, AF22342; AAP7982.1;

GO, GO:001642; AR79832.1;

GO, GO:0016494; F:C-X-C chemokine receptor activity; IEA.

GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.

GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

InterPro; IPR0040709; CXC. 3 receptor.

InterPro; IPR0040709; CXC. 3 receptor.

InterPro; IRR0040709; GXC. 3 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 NQAETHAWFISRFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20286573; PubMed=10825390;
Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S.,
Sarau H.M.;
Cytoplasmic (Potential).

By similarity.
N-linked (GlcNac. .) (Potential)
N-linked (GlcNAc. .) (Potential)
029FBB77BE3CD4EA CRC64;
                                                                                                                                 31.4%; Score 614; DB 1; Length 367; 38.8%; Pred. No. 3.4e-34; ive 58; Mismatches 139; Indels
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Last annotation update)
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PRINTS; PRO1532; CXCCHMKINER3.
PRINTS; PRO1537; GPCRHODOPSN.
PROSITE; PSO10237; G_PROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                      ilarity 38.8%;
Conservative 5
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321
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367 AA;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 NESDFSDSPPCPQ---DFSLNFDRTFLPVLYSLLFLLGLIGNGAVAAVLLSQRTALSSTD 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 FFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGV
                                                                                                                                                Gaps
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MEDLINE=22557679; PubMed=12671740;
Kuroda N., Uinuk-Ool T.S., Sato A., Samonte I.E., Figueroa F.,
Mayer W.E., Klein J.;
"Identification of chemokines and a chemokine receptor in cichlid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petromyzon marinus (Sea lamprey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
                                                                                                                                                14;
                                                                                             DB 2; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 KFRSDLSRLLTKLGCT---GPASLCQLFPSWRRSSLSESENATSL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 KFKEOMMMLLMRLGRSDORGPOR--OPSSSRRESSWSETTEASYL 365
                                                                                                                 %; Pred. No. 4e-34;
58; Mismatches 139; Indels
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 367 AA; 40934 MW; F67C0362EDDBFCB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP P1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                         ::
                                                                                                Score 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PRINTS; PRO0645; CXCCHMKINER4.
PRINTS; PRO0237; GPCRRHODOPSN.
                                                                                                31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                             Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemokine receptor CXCR4.
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60 GNSLVMLVILHSRVGRSVTDVYLLNLAMADLLFALTLPIWAAAKKNGWIFGTFLCKVVSL 119
                                                                                                                                                                                                                                                                                  188 AKVSQGHHNNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLLPMLVMGWCYVGVVHRLR 246
                                                                                                                                                                                                                                                                                                                                                                           247 QAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 CEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSLSESENA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 TELLGILHSCINPIIYAFIGQKFRHGILKILATHGLISKDSLPK---DSRPSFVGSSSGH 350
                  67
                                         GNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIA 127
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                                                                                                                                                                                                                                                                                                                                                                                                  MDLENLEDLFWELDRLDNYNDTSLVENHLCPATE-GPLMASFKAVFVPVAYSLIFLLGVI
                                                                                                                                                                                               128 LHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILF
                                                                                                                                                                                                                                                                                                                               179 RRIVYPTYIS--PVCYEDMGN--NTAKWRWURILPQTFGFILPLLIMLFCYGFTLRTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 MDLENLEDLFWELDRIDNYNDTSLVENHLCPATE-GPLMASFKAVFVPVAYSLIFLLGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
30.8%; Score 601.5; DB 2; Length Best Local Similarity 38.6%; Pred. No. 2.4e-33;
Matches 141; Conservative 57; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (Chimparase).
101-MAR-2004 (Chimparase).
101-MAR-2004 (Chimparese).
101-MAR-2004 (Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40122 MW; 809AB63ADA6A42C6 CRC64;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEPTOT; Transmembrane
SEQUENCE 355 AA; 40122 WW; 809AB63ADA6A42CG CRC(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00427; INTRLEUKINBR.
PRINTS; PR00573; INTRLEUKNBBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Q8HZN8
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                                                                                                                                                                                                                      72 VLVILERHROTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKV 131
                                                                                                                                                                                                                                                                  129
                                                                                                                                                                                                                                                                                                              132 NFYCSSLLLACIAVDRYLAIVHAVHAYHRRLLSIHITCGTIWLVGFLLALPEILFAKV- 190
                                                                                                                                                                                                                                                                                                                                        130 NLASSILLLACISIERYLAIVRATKTDKVRRKFATKVTCGAVWALSLLLAMPDLVFSHVY 189
                                                                                                                                                                                                                                                                                                                                                                                                     ---SQGHH--NNSLPRCTFSQENQAETHAWFTS-RFLYHVAGFLLPMLVMGWCYVGVVHR 244
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004872; F:interleukin-8 receptor activity; IEA.
GO, GO:0004872; F:receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001585; P:chemotaxis; IEA.
GO, GO:0007186; P:Chemotaxis; IEA.
InterPro; IPR000276; GFCR Rhodopsin.
InterPro; IPR000057; ILBB receptor.
InterPro; IRR000174; ILB_receptor.
                                                                                                                                                         10 LDEADLLPMGLNDTSELEDNPPRPAATAPTCLAPSQSFHRVFLPVVYGLVCLLGFAGNGL
                                                                                                                                                                                                                                                21 LDRLD----NYNDTS-LVENHLCPATEGPL----MASFKAVFVPVAYSLIFLLGVIGNVL
                                                                                        Gaps
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O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 8 receptor B CXCR2.
Cercopithecus pygerythrus (Vervet monkey).
Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Prinates; Catarrhini; Cercopithecinae; Cercopithecus.
                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                         31.1%; Score 607; DB 2; Length 374; 40.2%; Pred. No. 1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 355;
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39.0%; Pred. No. 1.2e-33;
ive 54; Mismatches 156; Indels
                                                                                      55; Mismatches 123; Indels
41113 MW; DEBD92B366776A0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 ITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 VAVTEGVGFSHCCFIPVLYAFVGKKFKENLARLRGCKACVG 341
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PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR00427; INTRLEUKINBR.

PROSITE; PS00523; INTRLEUKINBR.

PROSITE; PS0237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; TAGE F1 1; 1.
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                                                                                      Conservative
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Best Local Similarity 39.0
Matches 142; Conservative
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374 AA;
                                                              Similarity
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                                                                               Matches 137;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
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                                       Query Match
                                                                   Local
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QBHZN4
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294 TEILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSL----PKDSRPSFVGSSSG 349
                                                                                                188 AKVSQGHHNNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLLPMLVMGWCYVGVVHRLR 246
                                                                                                         : : | | | | : | | | | : | 179 RRTV--YSSNVSPACYEDMGN--NTANWRMLLRILDPQSFGFIVPLLIMLFCYGFTLRTLF 234
                                                                                                                                                                     307 CEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSLSESENA 366
Rearch completed: August 29, 2005, 23:56:59
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350 HTSTT 354
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Sequence 19, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 74, Appl
Sequence 7, Appl
Sequence 7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNWENTS

HESULT 1
US-08-202-056-5
i Sequence 5, Application US/08202056
j Patent No. 5440021
i GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
i APPLICANT: Hebert, Caroline
i APPLICANT: Lee James
i TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
                                     Sequence
Sequence
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100.0%; Pred. No. 8.7e-176;
tive 0; Mismatches 0;
US-09-409-778-4
US-08-153-848-19
US-09-29-843A-19
US-09-29-11153-19
US-08-133-11153-19
US-08-13-848-15
US-09-251-545-1
US-09-299-843-15
US-09-11153-15
US-09-11153-15
US-09-11153-17
US-09-139-843A-7
US-09-299-843A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION 136
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 amino acids
amino acid
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Best Local Similarity 100.(
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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200, App
6, Appli
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2, Appli
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1 MNYPLTLEMDLENLEDLFWE......PSWRRSSLSESENATSLTTF 372
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'GqD2 6/ptodata1/jaa/6A_COMB.pep:*
'GqD2 6/ptodata1/jaa/6B_COMB.pep:*
'GqD2 6/ptodata1/jaa/BCOMB.pep:*
'GqD2 6/ptodata1/jaa/PCTUS COMB.pep:*
'GqD2 6/ptodata1/jaa/backfiles1.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-170-496D-200
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Listing first 45 summaries
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121 LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLL 180
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GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.

TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                          Indels
                                                                              100.0%; Score 1953; DB 1;
100.0%; Pred. No. 8.7e-176;
tive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFCATION: 424
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APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
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Patent No. 5776457
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Best Local Similarity 100.
Matches 372; Conservative
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   TOPOLOGY: Linear
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US-08-076-093A-6
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Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kin, K.
TITLE OF INFORTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USAGE
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA: MS-DOS
RILING DATE: 11-Jun-1993
CLASSIFICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/81078
FILING DATE: 19-DEC-1991
FILIN
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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181 ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
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; Sequence 6, Application US/08805478
; Patent No. 584543
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Hebert, Caroline
; APPLICANT: Jimes
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; UNMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
 ADDRESSES: Genentech, Inc.
   STREET: 460 Point San Bruno Blvd
   CITY: South San Francisco
   STATE: California
   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1953; DB 2; Best Local Similarity 100.0%; Pred. No. 8.7e-176; Matches 372; Conservative 0; Mismatches 0;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELERAX: 415/25-5530
TELERAX: 415/25-5630
TELERAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 analno acids
"""" A maino Acid
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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100.0%; Pred. No. 8.7e-176;
vative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Hu
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
             REGISTRATION NUMBER: 34,659
REPERRINCE/DOCKET NUMBER: 706P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08284586
Patent No. 5840856
                                                                                                                                                                                     LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 SESENATSLTTF 372
                                                                                                                                                                                                                                                                                                                                         Matches 372; Conservative
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61 IFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF 120
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APPLICANT: Wood, William I.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR NUMBER OF SEQUENCES:

GORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 8.7e-176;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 1-JUN-1993
PRIOR APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTONNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPRAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 372 amino acids
Amino Acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESENATSLITE 372
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Best Local Similarity 100.
Matches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                         COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Control of the Compatible of the Compatible of the Control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                        CURRENT APPLICATION Genentecn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 11-UN-1993
PRIOR APPLICATION NUMBER: 07/810782
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P0706P2P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-802-627A-6; Sequence 6, Application US/08802627A; Patent No. 5822017; GENERAL INFORMATION: APPLICANT: Lee, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 372; Conservative
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                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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TOPOLOGY: Linear
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241 VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
                                                                                                     301 PVAITMCEFIGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
                                                                          301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
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                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08801228
Patent No. 5922541
GENERAL INFORMATION:
APPLICANT: Mood, William I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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SOCTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,228
FILING DATE: 19-Feb-1997
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRAR:
APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
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Amino Acid
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Best Local Similarity 100.
Matches 372, Conservative
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US-08-801-228-6
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US-08-801-228-6
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100.0%; Pred. No. 8.7e-176;
ive 0; Mismatches 0;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,238
FILING DATE: 19-Peb-1997
CLASSIFCATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
                                                                                                          Sequence 6, Application US/08801238
Patent No. 5919896
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I
TITLE OF INVENTION: PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetiech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
CITY: California
COUNTRY: USA
ZIP: 94080
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APPLICATION NUMBER: 07/810782
PILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERRNCE/DOCKET NUMBER: P0706PY
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415/225-5530
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
  361 SESENATSLTTF 372
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Best Local Similarity 100.0
Matches 372; Conservative
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LENGTH: 372 amino acic
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121 LCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLL 180
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                                                                                           Gaps
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    Length 372;
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US-08-982-493-8
US-08-982-493-8
Sequence 8, Application US/08982493
Sequence 8, Application US/08982493
Setent No. 6110695
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,493
FLING DATE:
CLASSIFICATION: 435
100.0%; Score 1953; DB 3;
100.0%; Pred. No. 8.7e-176;
tive 0; Mismatches 0;
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NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCSF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (650) 343-4341
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 372; Conservative
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    181 ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: OF COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: CAPUTER: CA
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/64228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION NUMBER: 08/076093
FILING DATE: 1-JUN-1993
PRIOR APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTONNEY, AGENT INPORMATION:
NAME: LOVE, RICHART B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
RECISTRATION NUMBER: 34,659
TELECOMMUNICATION:
TELEPHONE: 415/555-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09104296
Patent No. 6087475
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, WIlliam I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES. 6
STREET: 1 DNA WAY
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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STATE: California
COUNTRY: USA
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Sequence 10255, Application US/09949016

Facent No. 681239
GENDEAL INCPEMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WIMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTIMARE: PRELSEE FREESE FOR WINDOWS VERSION 4.0
SEQ ID NO 10255
LENGTH: 378
                                                                       PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
                                                                                                                                                                    301 PVAITWCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL 360
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 7 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAXSL
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100.0%; Score 1953; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.9e-176;
Matches 372; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               361 SESENATSLTTF 372
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Patent No. 655539
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: No. 6555339-Endogenous, CONSTITUTION OF INVENTION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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                                                       Length 372;
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                                                  Query Match 100.0%; Score 1953; DB 3; Best Local Similarity 100.0%; Pred. No. 8.7e-176; Matches 372; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1953; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESENATSLITE 372
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, MOLECULE TYPE: protein US-08-982-493-8
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CORGANISM: Homo sapiens
US-09-170-496D-66
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US-09-170-496D-66
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119 TFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGF 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLIFLLGMMGNILVLVILERHRHTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLG
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Sequence 2, Application US/08709838

Patent No. 6140064

GENERAL INFORMATION:

APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 374;
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COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patent Floors Miss.
SOFTWARE: Patent Floors Miss.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,493
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COSMAN, RICHARD A
REGISTRATION NUMBER: 36,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.7%; Score 1635; DB 3;
82.9%; Pred. No. 7.5e-146;
ive 29; Mismatches 33;
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UCSF798-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 82.9%
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-982-493-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-709-838-2
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STATE:
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                                                                                                                                        APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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Pred. No. 3.2e-175;
0; Mismatches 1; Indels C
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; Retent No. 6110695
; GENERAL INFORMATION:
APPLICANT: Gunn, Michael D
APPLICANT: Williams, Lewis T
APPLICANT: Cyeter, Jason G
TITLE OF INVENTION: Modulating B Lymphocyte Chemokine
TITLE OF INVENTION: Receptor Interactions
NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                  US-09-170-496D-200
; Sequence 200, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%;
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Best Local Similarity 99.7
Matches 371; Conservative
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US-09-170-496D-200
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STATE: CALIFORNIA
COUNTRY: USA
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LENGTH: 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.5%; Score 635; DB 3; Length 368;
Best Local Similarity 40.8%; Pred. No. 9.9e-52;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps
                              COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David B.
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 861-6240
TELEFAN: (617) 861-6240
TELEFAN: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-709-838-2
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Search completed: August 29, 2005, 23:58:34 Job time : 44 secs

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8, Appli 8, Appli 10, Appl

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Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

Database :

25, Appl 7, Appli 2394, Ap 29, Appl

Sequence

Sequence Sequence Seguence

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US-10-239-423-78
US-10-2411-284-4
US-10-949-135-34
US-10-949-135-34
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US-10-911-381-174
US-10-106-698-6402
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US-10-131-385-174
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US-10-331-583-882
US-10-331-413-77
US-10-233-423-77
US-10-233-563-39
US-10-237-563-39
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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US-09-104-063-6

i Sequence 6, Application US/09104063

j Patent No. US20020163356A1

GENERAL INFORMATION:

APPLICANT: Lee, James

APPLICANT: Wood, William I.

TILLE OF INVENTION: PPF4A Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco

CONNEY: USA

ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
PILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/66428
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
PILING DATE: 11-JUN-1993
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       Sequence 80, Appl
Sequence 6, Appli
Sequence 2243, Ap
Sequence 154, App
Sequence 154, App
Sequence 74, Appl
Sequence 74, Appl
Sequence 59, Appl
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                                                                                                                                                     August 29, 2005, 23:51:16 ; Search time 164 Seconds (without alignments) 891.272 Million cell updates/sec
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1953
1 MNYPLTLEMDLENLEDLFWE .......PSWRRSSLSESENATSLTTF 372
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1: /cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/RSO7_NEW PUB.pep:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-225-567A-60
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US-10-251-385-20
US-11-021-951-154
US-10-251-385-20
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Score

Result No.

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RESULT 3

US-10-225-567A-60

i Sequence 60, Application US/10225567A

i Publication No. US20030113798A1

i GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences

APPLICANT: Burmer, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTC

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 60/257,144

MUMBER OF SEQ ID NOS: 2292

NUMBER OF SEQ ID NOS: 2292

SOFTWARE PATENTIN Version 3.1
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Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0;
                                                     3; DB 14; Length 372;
1.6e-165;
                                                                                                Indels
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                                                     100.0%; Score 1953;
100.0%; Pred. No. 1.6
tive 0; Mismatches
                                                     Query Match
Best Local Similarity 100.0
Matches 372; Conservative
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LENGTH: 372
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Sequence 66, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Proceedin-Coupled
TITLE OF INVENTION: Receptors
FILE REPRESENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT APPLICATION NUMBER: US/09/170,496
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR PLING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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                                                                                                                                           P0706P2C2
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHAR B.
RECISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P
TELECOMMUNICATION INFORMATION:
TELEFAM: 415/952-981
TELEFAM: 910/371-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             LENGTH: 372 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-104-063-6
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LENGTH: 372
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                                                                                                                                                                                                                                 APPLICANT: Mood, William I.

APPLICANT: Wood, William I.

ITLE OF INVENTION: Human PP4A Receptors, Nucleic Acid Encoding and TITLE OF INVENTION: Human PP4A Receptors, Nucleic Acid Encoding and TITLE OF INVENTION: Human PP4A Receptors, Nucleic Acid Encoding and TITLE OF INVENTION: Human PP4A Receptors, CURRENT APPLICATION NUMBER: US/10/66,689

CURRENT APPLICATION NUMBER: US/09/91/4,063

PRIOR APPLICATION NUMBER: US/09/104,063

PRIOR FILING DATE: 1996-08-25

PRIOR PILING DATE: 1996-08-26

PRIOR PLING DATE: 1996-08-26

PRIOR APPLICATION NUMBER: US/08/076,093

PRIOR PILING DATE: 1993-06-11

PRIOR PILING DATE: 1991-12-19

PRIOR APPLICATION NUMBER: US/07/677,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPEILFAKVSQGHINNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
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100.0%; Pred. No. 1.6e-165;
ative 0; Mismatches 0;
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US-10-276-774-2243
; Sequence 2243, Application US/10276774
                                                                                                                                                                    Sequence 6, Application US/10666689
Publication No. US20040037830A1
GENERAL INFORMATION:
                                361 SESENATSLTTF 372
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Best Local Similarity 100.
Matches 372, Conservative
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APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Coll Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
FILE REFERENCE: 022217us
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
FILE REFERENCE: 2002-03-23
FRIOR FILING DATE: 2000-03-31
FRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 80
LENGTH: 372
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                         ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
                                                                                             VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
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OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-80
ALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
                                                                                                                         VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/10239423
Publication No. US20030186889A1
GENERAL INFORMATION:
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US-10-239-423-80
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Publication No. US20050175891A1

GENERAL INFORMATION:

APPLICANT: HAUPTS, Ulrich

APPLICANT: SCHEIDIG, Andreas

APPLICANT: SCHEIDIG, Andreas

APPLICANT: WOTSMEIER, Christian

APPLICANT: Scheling, Ulrich

APPLICANT: WOTSMEIER, Christian

FILLE REFERENCE: 04156.0002U5

CURRENT PELING DATE: 2004-06-18

PRIOR PELING DATE: 2004-02-11

PRIOR PELING DATE: 2003-11-22

PRIOR FILING DATE: 2003-11-21

PRIOR FILING DATE: 2003-11-11

PRIOR PELING DATE: 2003-11-11

PRIOR FILING DATE: 2003-11-11

PRIOR PILING DATE: 2003-11-11

PRIOR PILING DATE: 2003-11-11

PRIOR PILING DATE: 2003-11-11

PRIOR FILING DATE: 2003-11-11

PRIOR PILING DATE: 2003-11-10

PRIOR PILING DATE: 2003-11-10

PRIOR PILING DATE: 2003-11-10
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                                                                                      Length 372;
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                                                                                   Query Match 99.7%; Score 1947; DB 14;
Best Local Similarity 99.7%; Pred. No. 5.4e-165;
Matches 371; Conservative 0; Mismatches 1;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 154
LENGTH: 371
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                       Homo sapiens
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ORGANISM: Homo sapiens
                       ; ORGANISM: Homo
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Sequence 200, Application US/10251385

Sublication No. US20030105292A1

GENERAL INFORMATION:

APPLICANT: Chalmers, Derek T.

CURRENT APPLICATION NUMBER: US/10/1251,385

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 200

LENGTH: 372
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                                   APPLICANT: Hyaeq, Inc.
APPLICANT: Tang, Y, Tom et al
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2243
LENGTH: 378
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Publication No. US20040053245A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 372; Conservative
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CRGANISM: Homo sapiens
US-10-276-774-2243
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US-10-251-385-200
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APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTC FILE REPERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PATENTIN VETBION 3.1
                                                                                                                                249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                                                                                                                                                                                                                                                                    245 SRGQRRIARAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 304
                                                                                                                                                                                                                                                                                                                                                                                                309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
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            133 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 190
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                                                                                    191 SQCHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA
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; Publication No. US20030148394A1
; PENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 74, Application US/10225567A, Publication No. US20030113798A1, GENERAL INFORMATION: APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-74
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US-10-345-680-59
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Publication No. US20030105292A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Protein-Coupled

TITLE OF INVENTION: Protein-Coupled

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Protein-Coupled

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                                                                                                                                                                                                                            1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
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                                                                            DB 20; Length 371;
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                                                                    Score 1938.5; DB 2.
Pred. No. 3.1e-164;
0; Mismatches 0;
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32.5%; Score 635; DB 14;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145;
                                                                        99.3%;
                                                                Query Match
Best Local Similarity 99.77
Matches 371; Conservative
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US-11-021-951-154
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TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLFLFLGLLGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 SQCHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 368;
                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREBT: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 635; DB 14;
40.8%; Pred. No. 4.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brook EBG., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/251,686 FILING DATE: 20-Sep-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-239-423-78
; Sequence 78, Application US/10239423
; Publication No. US20030186889A1
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-624
TELEFAX: (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.8<sup>3</sup>
Matches 147; Conservative
                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-251-686-2
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                   ### APPLICANT: Venkaceswarlu, Karicheti
#### APPLICANT: Venkaceswarlu, Karicheti
##### TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
##### TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
#### TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
#### TITLE OF INVENTION: 641, 260, 50899, 21407, 42032, 46656, 62553, 302, 323,
### TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
### TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
### TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
### CURRENT FILING DATE: 2002-01-18
### PRIOR FILING DATE: 2002-01-18
### PRIOR FILING DATE: 2002-03-15
### PRIOR FILING DATE: 2002-04-19
### PRIOR FILING DATE: 2002-04-19
### PRIOR FILING DATE: 2002-08-14
### PRIOR FILING DATE: 2002-08-14
### PRIOR FILING DATE: 2002-02-2
### PRIOR FILING DATE: 2002-02-2
### PRIOR FILING DATE: 2002-02-2
### PRIOR FILING DATE: 2002-01-1
### PRIOR FILING DATE: 2002-01-2
### PRIOR FILING DATE: 2002-01-02
### PRIOR FILING DATE: 2002-11-05
### PRIOR FILING DATE: 2002-01-02
### PRIOR FILING DATE: 2002-01-02
### PRIOR FILING DATE: 2002-01-02
### PRIOR FILING DATE: 2002-01-05
### PRIOR FILING DATE: 2002-00-10-05
### PRIOR FILING DATE: 2002-01-05
### PRIOR FILING DATE: 2002-00-10-05
### PRIOR FILING DATE: 2002-01-05
### PRIOR FILING DATE: 2002-00-10-05
### PRIOR FILING DATE: 2002-00-10-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORRPOROKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24S SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENFSSSY----DYGENESD-SCCTSPPCPQ----DFSLNFDRAFLPALYSLLFLLGLLGNG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.5%; Score 635; DB 14; Length 368; 40.8%; Pred. No. 4.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.2e-48; ; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Loetscher, Marcel
Moser, Bernhard
Qin, Shixin
Mackay, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10251686 Publication No. US20030158392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi:
Matches 147; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-345-680-59
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PILING DATE: 2002-02-08
APPLICATION NUMBER: US 60/356,714
PILING DATE: 2002-02-13
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Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                   Matches 147; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                  Query Match
Best Local Similarity
                                           US-10-411-284-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
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             APPLICANT: FORSEMANN, Wolf-Georg; FORSEMANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Protecome of Tunor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REPRENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
FRIOR APPLICATION NUMBER: DE10016013.1
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLIGLIGNG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10411284;
Sequence 4, Application US/10411284;
Publication No. US20030224426A1
GENERAL Involvantion:
APPLICANT: Li, Yi
ITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REPERENCE: PP218P1
CURRENT APPLICATION NUMBER: US/10/411,284
CURRENT FILING DATE: 2003-04-11
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 1998-12-21
PRIOR PELICATION NUMBER: 09/101,518
PRIOR PELICATION NUMBER: 09/101,518
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-01-11
SHOR PLING DATE: 1986-01-11
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver: 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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SEQ ID NO 78
LENGTH: 368
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191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
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                                                                                                                                                                                                                                                                                                                    71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Sob Biotechnology, Inc.
TITLE OF INVENTION NUMBER: US/10/295,027
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR PLILING DATE: 2001-11-29
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-12-14
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PRIOR PLILING DATE: 2002-01-08
PRIOR PRILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-08
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                                                                                                                                                          11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV
                                                                                   Gaps
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        Length 368;
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32.5%; Score 635; DB 15; 40.8%; Pred. No. 4.2e-48; tive 50; Mismatches 145;
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APPLICATION NUMBER: US 60/355,250
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71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
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32.5%; Score 635; DB 15; Length.368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SEQ TWARE: PatentIn Ver. 2.1
SEQ ID NO 752
LENGTH: 368
TURGE: PRI
CRGANISM: Homo sapiens
US-10-295-027-752
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Search completed: August 30, 2005, 00:01:24 Job time : 166 secs